

Table S1: Real-time quantitative RT-PCR primers of unpublished genes. Gene names are given based on similarities with *Arabidopsis* genes. Homologies are given in percentage of identities after blast of the peptide sequences in <http://www.arabidopsis.org> for *Arabidopsis* genes.

Gene name (based on At similarities)	Sequence used for primer design	Peptidic homology with <i>Arabidopsis</i> <i>thaliana</i> (% of identities)		Primer sequences for qPCR	Expression localisation in rose
<i>RhCKX6</i>	Rc001490*	AT3G63440	76%	GCAGCACCTGCAAGGGTAAA	bud
				CTCGGGTAAATGCTGCGAAA	
<i>RhLOG3</i>	RC046428*	AT2G37210	66%	AGGCCAAGAGCTGGTGTCAA	bud
				AGTCCAATGCTTCACCTCCA	
<i>RhLOG8</i>	Rc046428*	At5g11950	79%	GTCGGGTTGATGGGTTGGT	apical stem and bud
				GGCATGAGAGCTTTGGAATGA	
<i>RhPUP5</i>	Rc018024*	AT2G24220	80%	TTCTTCTACTTCTAACGAGTCGGC	apical stem and bud
				CCCTGCAACAGCCACCCATG	
<i>RhSWEET10</i>	Rc000972*	AT5G50790	53%	AGCCAAGCAAGGTTCAAGGAGC	apical stem and bud
				TGGGGTCAGGTCTGGACACAC	
<i>RhCYD3;1</i>	Rc010500*	AT4G34160	54%	GCTTCACCGCTCTCATCTTGCC	apical stem and bud
				TGCGAAGGCCTGAAGTCTGCT	
<i>RhPCNA1</i>	Rc001162*	AT1G07370	89%	TCGCACACAGTCACTATCAGCCT	apical stem and bud
				ACCTTCGGAGCCAAGTAGAACCT	
<i>RhARR3</i>	Rc004606*	AT1G59940	88%	CGGAGGAGGTCGGACAAGCT	apical stem and bud
				AGGACGTGAGCTTCTCGGAACT	
<i>RhARR5</i>	Rc010901*	AT3G48100	79%	TGGGATGACAGGATATGAGCTGCT	apical stem and bud
				CTCTGAGGACATGATCACCACTGG	
<i>RhENT1</i>	Rc018452*	AT1G70330	67%	AATGTGGACCGAGGATTCCG	apical stem and bud
				TCGATCTAACACAGACCCCCGT	
<i>RhEXP</i>	Degenerate primers	AT1G69530	59%	GCCAAGGCTATGGGACTAACAC	bud
				GAGCTCATAACATGCTCCACAAGT	
<i>RhSUSY</i>	EC 2.4.1.13	AT5G20830	83%	AAAGACCCTCTCACTGGGACAAG	apical stem and bud
				CCAGTCAGGTCAAGAGCCTTCA	

* clusters identified in the *Rosa chinensis* database iant.toulouse.inra.fr/R.chinensis